Improvement of virus resistance breeding in barley by the help of *H. bulbosum*

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Hordeum bulbosum, the only member in the secondary genepool of *Hordeum vulgare*, holds resistances and tolerances against various pathogens, for example against *Barley mild mosaic virus*/*Barley yellow mosaic virus* (BaMMV/BaYMV) or *Barley yellow dwarf virus* (BYDV). Both diseases cause high yield losses in barley. Furthermore, the control of the aphid-transmitted BYDV is becoming difficult due to governmental regulations concerning insecticides. The use of chemicals to control BaMMV/BaYMV, transferred by the soil-borne protist *Polymyxa graminis*, is not possible. Thus, breeding for resistance is the only possibility to protect barley against these diseases.

Different *H. bulbosum* introgression lines carrying resistance against BaMMV/BaYMV (*Rym16*^{Hb}) and tolerance against BYDV (*Ryd*$_{203S11}$^{Hb}) on chromosome 2HL were characterized. The sizes of the introgression fragments were calculated based on the barley reference sequence and resulted in a size of 4.2 Mb for the locus *Ryd*$_{203S11}$^{Hb} and 3 Mb for the locus *Rym16*^{Hb}.

The analysis of 10.000 F_2 plants carrying *Ryd*$_{203S11}$^{Hb} and 4440 F_2 plants carrying *Rym16*^{Hb} with co-dominant flanking markers resulted in 34 recombinant F_3 plants, which will be used to construct high resolution mapping populations. The recombination rate within the introgression is about 14 times reduced compared to the intraspecific recombination rate within in the barley genome, most likely caused by the incomplete homology between the genome of *H. vulgare* and *H. bulbosum*.

As a basis for isolating the respective genes via a map-based cloning approach, recombinant plants will be selfed, phenotyped and saturated with markers using Exome capture, GBS and Illumina 50K data. A non-gridded BAC library will be used to construct a physical map of the target region of *Ryd*$_{203S11}$^{Hb}. This map will help to identify candidate genes located in the *H. bulbosum* introgression fragment. In addition, the resistance of *Rym16*^{Hb} will be analyzed by using resistance gene enrichment sequencing (RenSeq).